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SEQ ID NO:

6	mouse_E3αI	MASEMEPEVQ	AI D- RSLLEC	SAEEI	AGRWL	QATDLNREVV	QHLAHCVPKI	49
4	human_E3αI	MASELEPEVQ	AI D- RSLLEC	SAEEI	AGKWL	QATDLTREVV	QHLAHYVPKI	49
15	mouse_E3αI	MADEEMDGAE	RMDVSPPEPL	APQRPASWMD	QQVDFYTAFL	HHLAQLVPEI		50
2	human_E3αI	MADEEAGGTE	RMEI SAELPQ	TPQRLASWMD	QQVDFYTAFL	HHLAQLVPEI		50
	Consensus	MA. E. ....	. D. .... L. .	. . . . . A. W.	Q. . D. . . . .	. HLA. . VP. I		50
6	mouse_E3αI	YCRGPNPFPQ	KEDTLAQHIL	LGPMEWVICA	EDPALGFPKL	EQANKPSHLC		99
4	human_E3αI	YCRGPNPFPQ	KEDMLAQHVL	LGPMEWVLCG	EDPAFGFPKL	EQANKPSHLC		99
15	mouse_E3αI	YFAEMDPDLE	KQEESVQMSI	LTPLEWVWLF	EDPDI CLEKL	KHSG- AFQLC		99
2	human_E3αI	YFAEMDPDLE	KQEESVQMSI	FTPLEWVWLF	EDPDI CLEKL	KHSG- AFQLC		99
	Consensus	Y. .... P. . . .	K. .... Q. . .	L. P. EWV. L. G	EDP. .... KL	. . . . . LC		100
6	mouse_E3αII	GRVFKVGEPT	YSCRDCAVDP	TCVLCMECFL	GSI HRDHRYR	MTTSGGGGFC		149
4	human_E3αII	GRVFKVGEPT	YSCRDCAVDP	TCVLCMECFL	GSI HRDHRYR	MTTSGGGGFC		149
15	mouse_E3αI	GKVFKSGETT	YSCRDCAI DP	TCVLCMDCFCQ	SSVHKNHRYK	MHTSTGGGFC		149
2	human_E3αI	GRVFKSGETT	YSCRDCAI DP	TCVLCMDCFCQ	DSVHKNHRYK	MHTSTGGGFC		149
	Consensus	GRVFK. GE. T	YSCRDCA. DP	TCVLCM CF. .	S. H. . HRY. M	TS. GGGFC		150
6	mouse_E3αII	DCGDTEAWKE	GPYCQKHKLS	SSEVVEEEDP	LVHLSedVI A	RTYNI FAI MF		199
4	human_E3αII	DCGDTEAWKE	GPYCQKHELN	TSEIEEEEDP	LVHLSedVI A	RTYNI FAI TF		199
15	mouse_E3αI	DCGDTEAWKT	GPFCVDHEPG	RAGTTKESLH	- CPLNEEVI A	QARRI FPSVI		198
2	human_E3αI	DCGDTEAWKT	GPFCVNHEPG	RAGTI KENS R	- CPLNEEVI V	QARKI FPSVI		198
	Consensus	DCGDTEAWK. GP. C. . HE. .	. . . . . E. . . .	. . . L. E. V. I A .	. . . I F. . . .			200

Figure 1B

6	mouse_E3 $\alpha$ II	RYAVDILTWE	KESELPEDLE	VAEKSDTYYC	MLFNDEVHTY	EQVIYTLQKA	249
4	human_E3 $\alpha$ II	RYAVEILTWE	KESELPADLE	MVEKSDTYYC	MLFNDEVHTY	EQVIYTLQKA	249
15	mouse_E3 $\alpha$ I	KYIVEMTIWE	EEKELPPELQ	I REKNERYYC	VLFNDEHHSY	DHVIYSLQRA	248
2	human_E3 $\alpha$ I	KYVVEMTIWE	EEKELPPELQ	I REKNERYYC	VLFNDEHHSY	DHVIYSLQRA	248
	Consensus	.Y.VE...WE	.E.ELP...L.	..EK...YYC	.LFNDE.H.Y	..VIY.LQ.A	250
6	mouse_E3 $\alpha$ II	VNCTQKEAIG	FATTVDRDGR	RPVRYGDFQY	CDQAKTIVIR	NTSRQTK-PL	298
4	human_E3 $\alpha$ II	VNCTQKEAIG	FATTVDRDGR	RSVRYGDFQY	CEQAKSVIVR	NTSRQTK-PL	298
15	mouse_E3 $\alpha$ I	LDCELAEACL	HTTAIDKEGR	RAVKAGVYAT	CQEAKEDIKS	HSENVSQHPL	298
2	human_E3 $\alpha$ I	LDCELAEACL	HTTAIDKEGR	RAVKAGAYAA	CQEAKEDIKS	HSENVSQHPL	298
	Consensus	..C...EA..	..T...D..GR	R.V..G....	C..AK..I..	.....PL	300
6	mouse_E3 $\alpha$ II	KVQVMHSSVA	AHQNFGLKAL	SWLGSVIGYS	DGLRRLCQV	GLQEGPDGEN	348
4	human_E3 $\alpha$ II	KVQVMHSSIV	AHQNFGLKLL	SWLGSII GYS	DGLRRLCQV	GLQEGPDGEN	348
15	mouse_E3 $\alpha$ I	HVEVLHSVVM	AHQKFALRLG	SWWNKIMSYS	SDFRQIFCQA	CLVEEPGSEN	348
2	human_E3 $\alpha$ I	HVEVLHSEIM	AHQKFALRLG	SWWNKIMSYS	SDFRQIFCQA	CLREEPDSEN	348
	Consensus	.V.V.HS...	AHQ.F.L.L.	SW...I...YS	...R.I.CQ.	.L.E.PD.EN	350

Figure 1C

6	mouse_E3 $\alpha$ II	SSLVDRMLN	DSKLWKGARS	VYHQLFMSSL	LMDLKYKKLF	ALRFAKNYRQ	398
4	human_E3 $\alpha$ II	SSLVDRMLS	DSKLWKGARS	VYHQLFMSSL	LMDLKYKKLF	AVRFAKNYQQ	398
15	mouse_E3 $\alpha$ I	PCLISRLMLW	DAKLYKGARK	ILHELIFSSF	FMEMEYKKLF	AMEFVKYYKQ	398
2	human_E3 $\alpha$ I	PCLISRLMLW	DAKLYKGARK	ILHELIFSSF	FMEMEYKKLF	AMEFVKYYKQ	398
	Consensus	. . L . . R L M L .	D . K L . K G A R .	. . H . L . . S S .	. M . . Y K K L F	A . . F . K . Y . Q	400
6	mouse_E3 $\alpha$ II	LQRDFMEDDH	ERAVSVTALS	VQFFTAPTLA	RMLTEENLM	TVI I KAFMDH	448
4	human_E3 $\alpha$ II	LQRDFMEDDH	ERAVSVTALS	VQFFTAPTLA	RMLTEENLM	SI I I KTFMDH	448
15	mouse_E3 $\alpha$ I	LQKEYISDDH	ERSISITALS	VQMLTVPTLA	RHLIEEQNVI	SVI TETLLEV	448
2	human_E3 $\alpha$ I	LQKEYISDDH	DRSISITALS	VQMFTVPTLA	RHLIEEQNVI	SVI TETLLEV	448
	Consensus	L Q . . . . . D D H	E R . . S . T A L S	V Q . F T . P T L A	R . L I . E . N . .	S V I . . T . . .	450

# Figure 1D

SEQ ID NO:							
6	mouse_E3αII	LKHRDAQGRF	QFERYTALQA	FKFRRVQS LI	LDLKYVLISK	PTEW5DEL RQ	498
4	human_E3αII	LRHRDAQGRF	QFERYTALQA	FKFRRVQS LI	LDLKYVLISK	PTEW5DEL RQ	498
15	mouse_E3αI	LPEYLD RNN-	KFN-FQYSQ	DKLGRVYAVI	CDLK YILISK	PVI WTER LRA	496
2	human_E3αI	LPEYLD RNN-	KFN-FQYSQ	DKLGRVYAVI	CDLK YILISK	PTI WTER LRM	496
	Consensus	L.....	F.....	. K.. RV... I	. DLKY. LISK	PT. W.. LR.	500
6	mouse_E3αII	KFLQGFDAFL	ELLKCMQGM D	PITRQVGQHI	EMEPEWEAAF	TLQM KLTHVI	548
4	human_E3αII	KFLEGFDAFL	ELLKCMQGM D	PITRQVGQHI	EMEPEWEAAF	TLQM KLTHVI	548
15	mouse_E3αI	QFLEGFRSFL	KILT CMQME	EIRRVQVGQHI	EVDPDWEAAI	AI QMQLKN I L	546
2	human_E3αI	QFLEGFRSFL	KILT CMQME	EIRRVQVGQHI	EVDPDWEAAI	AI QMQLKN I L	546
	Consensus	. FLEGF.. FL	.. L. CMQGM	. I. RVQVGQHI	E.. P. WEAA.	.. QM L....	550
6	mouse_E3αII	SMVQDWCALD	EKVLI EAYKK	CLAVLTQCHG	GFTDGEQPI T	LSI CGHSVET	598
4	human_E3αII	SMMQDWCASD	EKVLI EAYKK	CLAVLMQCHG	GYTDGEQPI T	LSI CGHSVET	598
15	mouse_E3αI	LMFQEWCACD	EDLLLVAYKE	CHKAVMRCST	NFM5STKT V-	VQLCGHSLET	595
2	human_E3αI	LMFQEWCACD	EELLLVAYKE	CHKAVMRCST	SFISSSKTV-	VQSCGHSLET	595
	Consensus	. M Q. WCA. D	E.. L.. AYK.	C.... M C..	. F.....	.. CGHS. ET	600

Figure 1E

6	mouse_E3 $\alpha$ II	I RYCVS	QEKV	SI HLP	ISRL	AGLHV	LSKS	EVAYK	FPELL	PLSEL	SPPM	648
4	human_E3 $\alpha$ II	I YCVS	QEKV	SI HLP	PVSRL	AGLHV	LSKS	EVAYK	FPELL	PLSEL	SPPM	648
15	mouse_E3 $\alpha$ I	KSYKV	SEDLV	SI HLP	PLSRTL	AGLHV	LSRL	GAI SRL	HEFV	PFDSF	QVEVL	645
2	human_E3 $\alpha$ I	KSYRV	SEDLV	SI HLP	PLSRTL	AGLHV	LSRL	GAUSRL	HEFV	SFEDF	QVEVL	645
	Consensus	..Y.VS...	V	SI HLP	.SR.L	AGLHV	.LS..	.....E..	P.....	L		650
6	mouse_E3 $\alpha$ II	I EHPL	RCLVL	CAQVH	AGMMR	RNGFS	LVNQI	YYYHN	VKCRR	EMFDK	DI VML	698
4	human_E3 $\alpha$ II	I EHPL	RCLVL	CAQVH	AGMMR	RNGFS	LVNQI	YYYHN	VKCRR	EMFDK	DVVM	698
15	mouse_E3 $\alpha$ I	VEYPL	RCLVL	VAQVVA	EAEMMR	RNGLS	LSI SQV	FYYQD	VKCRE	EMYDK	DI I ML	695
2	human_E3 $\alpha$ I	VEYPL	RCLVL	VAQVVA	EAEMMR	RNGLS	LSI SQV	FYYQD	VKCRE	EMYDK	DI I ML	695
	Consensus	.E.PLR	RCLVL	.AQV.A	.MMR	RNG.SL..	Q..YY..	VKCR.	EM	DKDI..	ML	700
6	mouse_E3 $\alpha$ II	QTGVSM	MDPN	HFLM	MSRF	ELYQL	FSTPD	YGKRF	SSEVT	HKDVV	QQNNT	748
4	human_E3 $\alpha$ II	QTGVSM	MDPN	HFLM	MSRF	ELYQL	FSTPD	YGKRF	SSEIT	HKDVV	QQNNT	748
15	mouse_E3 $\alpha$ I	QI GAS	MDPN	KFLLL	VLQRY	EL-----	TDA	FNKTI	ST--K	DQDLI	KQYNT	738
2	human_E3 $\alpha$ I	QI GAS	MDPN	KFLLL	VLQRY	EL-----	AEA	FNKTI	ST--K	DQDLI	KQYNT	738
	Consensus	Q.G.S.	MDPN	.FL...L.R.	EL.....T...	..K..S.....	..D...Q.NT					750

Figure 1F

6	mouse_E3 $\alpha$ II	LI E E M L Y L I I	M L V G E R F N P G	V G Q V A A T D E I	K R E I I H Q L S I	K P M A H S E L V K	798
4	human_E3 $\alpha$ II	LI E E M L Y L I I	M L V G E R F S P G	V G Q V N A T D E I	K R E I I H Q L S I	K P M A H S E L V K	798
15	mouse_E3 $\alpha$ I	LI E E M L Q V L I	Y I V G E R Y V P G	V G N V T R E E V I	M R E I T H L L C I	E P M P H S A I A R	788
2	human_E3 $\alpha$ I	LI E E M L Q V L I	Y I V G E R Y V P G	V G N V T K E E V T	M R E I I H L L C I	E P M P H S A I A K	788
	Consensus	LI E E M . . . I	. . V G E R . . P G	V G . V . . . . . I	. R E I I H . L . I	. P M H S . . . K	800
6	mouse_E3 $\alpha$ II	S L P E D E N K E T	G M E S V I E S V A	H F K K P G L T G R	G M Y E L K P E C A	K E F N L Y F Y H F	848
4	human_E3 $\alpha$ II	S L P E D E N K E T	G M E S V I E A V A	H F K K P G L T G R	G M Y E L K P E C A	K E F N L Y F Y H F	848
15	mouse_E3 $\alpha$ I	N L P E N E N N E T	G L E N V I N K V A	T F K K P G V S G H	G V Y E L K D E S L	K D F N M Y F Y H Y	838
2	human_E3 $\alpha$ I	N L P E N E N N E T	G L E N V I N K V A	T F K K P G V S G H	G V Y E L K D E S L	K D F N M Y F Y H Y	838
	Consensus	. L P E . E N . E T	G . E . V I . . V A	. F K K P G . . G .	G . Y E L K . E . .	K . F N . Y F Y H .	850
6	mouse_E3 $\alpha$ II	S R A E Q S K A E E	A Q R K L K R E N K	E D T A L P P P A L	P P F C P L F A S L	V N I L Q C D V M L	898
4	human_E3 $\alpha$ II	S R A E Q S K A E E	A Q R K L K R Q N R	E D T A L P P P V L	P P F C P L F A S L	V N I L Q S D V M L	898
15	mouse_E3 $\alpha$ I	S K T Q H S K A E H	M Q K K R R K Q E N	K D E A L P P P P P	P E F C P A F S K V	V N L L S C D V M	888
2	human_E3 $\alpha$ I	S K T Q H S K A E H	M Q K K R R K Q E N	K D E A L P P P P P	P E F C P A F S K V	I N L L N C D I M M	888
	Consensus	S . . . . S K A E .	. Q . K . . . Q . .	. D . A L P P P . .	P . F C P . F . . .	V N . L . C D V M	900

Figure 1G

SEQ ID NO:							
6	mouse_E3αII	YI MGTI LQWA	VEHGSWSE	SMLQRVLHLI	GMALQEEKHH	LENAVEGHVQ	948
4	human_E3αII	CI MGTI LQWA	VEHNGYAWSE	SMLQRVLHLI	GMALQEEKQH	LENVTEEHVV	948
15	mouse_E3αI	YI LRTI FERA	VDTESNLWTE	GMLQMAFHI L	ALGLLEEKQQ	LQKAPEEEV-	937
2	human_E3αI	YI LRTVFERA	I DTDSNLWTE	GMLQMAFHI L	ALGLLEEKQQ	LQKAPEEEV-	937
	Consensus	YI..TI...A	V.....WE	.MLQ...H..	...L.EEKQ.	L..A.EE.V.	950
6	mouse_E3αII	TFTFTQKI SK	PGDAPHNSPS	I LAMLETQN	APSLAETHKDM	IRWLLKMFNA	998
4	human_E3αII	TFTFTQKI SK	PGEAPKNPS	I LAMLETQN	APYLEVHKDM	IRW LKTFNA	998
15	mouse_E3αI	AEDFYHKASR	LGSSAMNAQN	I QMLERLKG	I PQLEGQKDM	ITW LQMFDT	987
2	human_E3αI	TFDFYHKASR	LGSSAMNI QM	L---LEKLKG	I PQLEGQKDM	ITW LQMFDT	984
	Consensus	TF.F..K.S.	.G....N..	I...LE.L..	.P.LE..KDM	I.W.L.MF..	1000
6	mouse_E3αII	I KKI RE--CS	SSSPVAEAE	TI MEESSRDK	DKAERKRKAE	I ARLRREKI M	1046
4	human_E3αI	VKKMRE--SS	PTSPVAETEG	TI MEESSRDK	DKAERKRKAE	I ARLRREKI M	1046
15	mouse_E3αI	VKRLREKSCL	VVATTSGLEC	I KSEIETHDK	EKAERKRKAE	AARLHRQKI M	1037
2	human_E3αI	VKRLREKSCL	I VATTSGSES	I KNDEIETHDK	EKAERKRKAE	AARLHRQKI M	1034
	Consensus	VK..RE..C.	.....E.	...EE...DK	.KAERKRKAE	.ARL.R.KI M	1050



Figure 1H

6	mouse_E3 $\alpha$ II	AQMSEMQRHF	IDENKELFQQ	TLELDTSASA	TL--DSSPPV	SDAALTALGP	1094
4	human_E3 $\alpha$ II	AQMSEMQRHF	IDENKELFQQ	TLELDASTA	VL--DHSPVA	SDMTLTALGP	1094
15	mouse_E3 $\alpha$ I	AQMSALQKNF	IETHKLMYDN	TSEVTGKEDS	IMEEESTSAV	SEASRIALGP	1087
2	human_E3 $\alpha$ I	AQMSALQKNF	IETHKLMYDN	TSEMPGKEDS	IMEEESTPAV	SDYSRIALGP	1084
	Consensus	AQMS...Q..F	I...K.....	T.E.....	.....S.P.V	SD....ALGP	1100
6	mouse_E3 $\alpha$ II	AQTQVPEPRQ	FVTCILCQEE	QEVTVGSRAM	VLAAFVQRST	VLSKDRTKTI	1144
4	human_E3 $\alpha$ II	TQTQVPEQRQ	FVTCILCQEE	QEVKVESRAM	VLAAFVQRST	VLSKNRSKFI	1144
15	mouse_E3 $\alpha$ I	KRGPAVTEKE	VLTCILCQEE	QEVKLENNAM	VLSACVQKST	ALTQHRGKPV	1137
2	human_E3 $\alpha$ I	KRGPSVTEKE	VLTCILCQEE	QEVKIENNAM	VLSACVQKST	ALTQHRGKPI	1134
	Consensus	.....	..TCILCQEE	QEVK.E..AM	VL.A.VQ.ST	.L...R.K.I	1150
6	mouse_E3 $\alpha$ II	AD-PEKYDPL	FMHPDLSCGT	HTGSCGHVMH	AHCWQRYFDS	VQAKEQRRQQ	1193
4	human_E3 $\alpha$ II	QD-PEKYDPL	FMHPDLSCGT	HTSSCGHI MH	AHCWQRYFDS	VQAKEQRRQQ	1193
15	mouse_E3 $\alpha$ I	DHLGETLDPL	FMDPDLAHGT	YTGSCGHVMH	AVCWQKYFEA	VQ---LSSQQ	1184
2	human_E3 $\alpha$ I	ELSGEALDPL	FMDPDLAYGT	YTGSCGHVMH	AVCWQKYFEA	VQ---LSSQQ	1181
	Consensus	....E..DPL	FM PDL..GT	.TGSCGHVMH	A.CWQ.YF..	VQ.....QQ	1200

Figure 1I

6	mouse_E3 $\alpha$ II	RLRLHTSYDV	ENGEFLCPLC	ECLSNVTI·PL	L-LPPRSILS	RRLN-FSDQP	1241
4	human_E3 $\alpha$ II	RLRLHTSYDV	ENGEFLCPLC	ECLSNVTI·PL	L-LPPRNIFN	NRLN-FSDQP	1241
15	mouse_E3 $\alpha$ I	RIHVDL-FDL	ESGEYLCPLC	KSLCNTVI·PI	IPLQPQKINS	ENAEALAQLL	1233
2	human_E3 $\alpha$ I	RIHVDL-FDL	ESGEYLCPLC	KSLCNTVI·PI	IPLQPQKINS	ENADALAQLL	1230
	Consensus	R.....D	E·GE·LCPLC	..L·NTVI·P·	..L·P·I·S	.....	1250
6	mouse_E3 $\alpha$ II	DLAQWTRAVT	QQI·KVVQMLR	RKHNAA-DTS	SSETEAMNI	IPI·PEGFRPD	1290
4	human_E3 $\alpha$ II	NLTQWRTIS	QQI·KALQFLR	KEESTP-NNA	STKNSENVDE	LQL·PEGFRPD	1290
15	mouse_E3 $\alpha$ I	TLARWQTVL	ARI·SGYNI·KH	AKGEAPAVPV	LFNQGMGDST	FEFHSILSFG	1283
2	human_E3 $\alpha$ I	TLARWQTVL	ARI·SGYNI·RH	AKGENP-IPI	FFNQGMGDST	LEFHSILSFG	1279
	Consensus	·LA·W·TV·	..I.....	·K...P-...	.....	.....	1300
6	mouse_E3 $\alpha$ II	FYPRNPYSDS	I·KEMLTTFGT	AAYKVGLKVH	PNEGDP·RPVI	LCWGT·CAYTI	1340
4	human_E3 $\alpha$ II	FRPKIPYSES	I·KEMLTTFGT	ATYKVGLKVH	PNEED·RPVI	MCWGS·CAYTI	1340
15	mouse_E3 $\alpha$ I	VQSSVKYSNS	I·KEMWLFAT	TIYRI·GLKVP	PDELD·PRVPM	MTWST·CAFTI	1333
2	human_E3 $\alpha$ I	VESSI·KYSNS	I·KEMWLFAT	TIYRI·GLKVP	PDERD·PRVPM	LTWST·CAFTI	1329
	Consensus	.....YS·S	I·KEM...F·T	..Y...GLKV·	P·E·D·PRVP·	..W·T·CA·TI	1350

[illegible]

Figure 1K

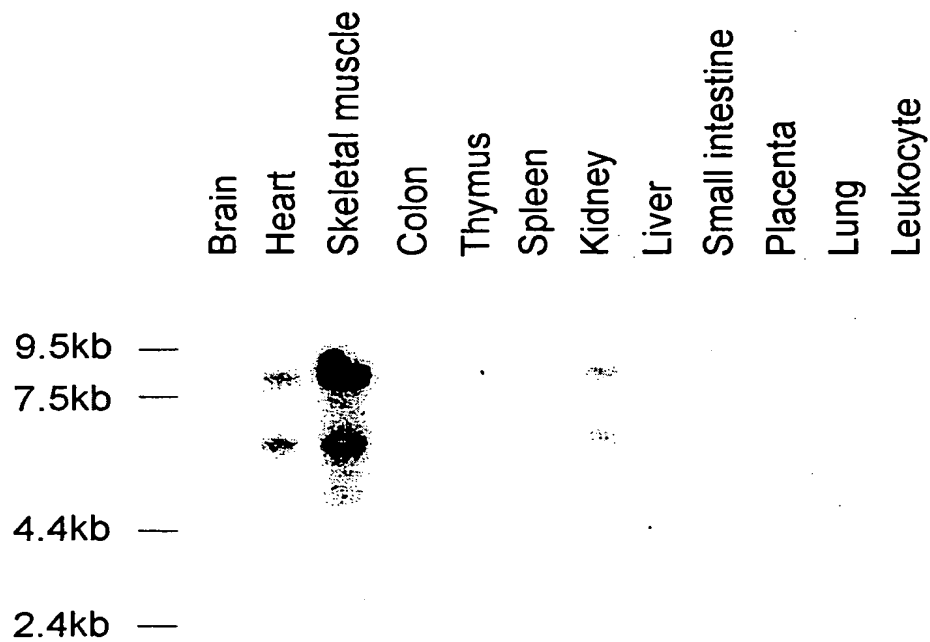
6	mouse_E3 $\alpha$ II	LHKTLLHQYTG	SALKEAPSGW	HLWRSVRAAI	MPFLKCSAL	FHYLNGVPAP	1532
4	human_E3 $\alpha$ II	LYKTLHQYTG	SALKEIPSGW	HLWRSVRAGI	MPFLKCSALF	FHYLNGVPSP	1532
15	mouse_E3 $\alpha$ I	FFVEVSQHTD	GLTGCGAPGW	YLWLSLRNGI	TPYLRC AALL	FHYLLGVAPP	1533
2	human_E3 $\alpha$ I	FFAEISQYTS	GSIGCDIPGW	YLWVSLKNGI	TPYLRC AALF	FHYLLGVTPP	1525
	Consensus	.....QYT.	.....GW	.LW.S.R.GI	.P.L.C.AL	FHYL.GV..P	1550
6	mouse_E3 $\alpha$ II	PDLQV-SGTS	HFEHLCNYLS	LPTNLHLFQ	ENS DIMNSLI	ESWCQNSEVK	1581
4	human_E3 $\alpha$ II	PDIQV-PGTS	HFEHLC SYLS	LPNNLICLFQ	ENSEIMNSLI	ESWC RNSEVK	1581
15	mouse_E3 $\alpha$ I	EELFANSAEG	EFSALCSYLS	LPTNLFLLFQ	EYWD TIRPLL	QRWCGDPALL	1583
2	human_E3 $\alpha$ I	EELHTNSAEG	EYSALCSYLS	LPTNLFLLFQ	EYWD TIRPLL	QRWCADPALL	1575
	Consensus	..L....S...	.F...LCSYLS	LPTNL..LFQ	E...D....L.	..WC.....	1600
6	mouse_E3 $\alpha$ II	RYLNGERGAI	SYPRGANKLI	DLPEDYSSLI	NQASNFSCPK	SGGDKSRAPT	1631
4	human_E3 $\alpha$ II	RYLEGERDAI	RYPRESNKLI	NLPEDYSSLI	NQASNFSCPK	SGGDKSRAPT	1631
15	mouse_E3 $\alpha$ I	KSLKQKSAVV	RYPRKRNSLI	ELPEDYSCLL	NQASHFRCPR	SADDERKHPV	1633
2	human_E3 $\alpha$ I	NCLKQKNTVV	RYPRKRNSLI	ELPDDYSCLL	NQASHFRCPR	SADDERKHPV	1625
	Consensus	..L.....	RYPR...N.LI	.LPEDYS.L.	NQAS.F.CP.	S...D....P.	1650

Figure 1L

6	mouse_E3 $\alpha$ II	LCLVCGSLLC	SQSYCCQAEI	EGEDVGACTA	HTYSCGSGAG	I FLRVRECQV	1681
4	human_E3 $\alpha$ II	LCLVCGSLLC	SQSYCCQTEL	EGEDVGACTA	HTYSCGSGVG	I FLRVRECQV	1681
15	mouse_E3 $\alpha$ I	LCLFCGAI LC	SQNI CCQEIV	NGEEVGACVF	HALHCGAGVC	I FLKI RECRV	1683
2	human_E3 $\alpha$ I	LCLFCGAI LC	SQNI CCQEIV	NGEEVGACIF	HALHCGAGVC	I FLKI RECRV	1675
	Consensus	LCL.CG..LC	SQ..CCQ...	.GE.VGAC..	H...CG.GV.	I FL..REC.V	1700
6	mouse_E3 $\alpha$ II	LFLAGKTKGC	FYSPPYLLDDY	GETDQGLRRG	NPLHLCQERF	RKI QKLWQQH	1731
4	human_E3 $\alpha$ II	LFLAGKTKGC	FYSPPYLLDDY	GETDQGLRRG	NPLHLCCKERF	KKI QKLWHQH	1731
15	mouse_E3 $\alpha$ I	VLVEGKARGC	AYPAPYLDEY	GETDPGLKRG	NPLHLSRERY	RKLHLVWQQH	1733
2	human_E3 $\alpha$ I	VLVEGKARGC	AYPAPYLDEY	GETDPGLKRG	NPLHLSRERY	RKLHLVWQQH	1725
	Consensus	....GK...GC	.Y..PYLD.Y	GETD.GL.RG	NPLHL...ER.	RK....WQQH	1750
6	mouse_E3 $\alpha$ II	SITEEI GHAQ	EANQTLVGI D	WQHL			1755
4	human_E3 $\alpha$ II	SVTEEI GHAQ	EANQTLVGI D	WQHL			1755
15	mouse_E3 $\alpha$ I	CIIEEI ARSQ	ETNQMLFGFN	WQLL			1757
2	human_E3 $\alpha$ I	CIIEEI ARSQ	ETNQMLFGFN	WQLL			1749
	Consensus	.I.EEI...Q	E.NQ.L.G..	WQ.L			1774

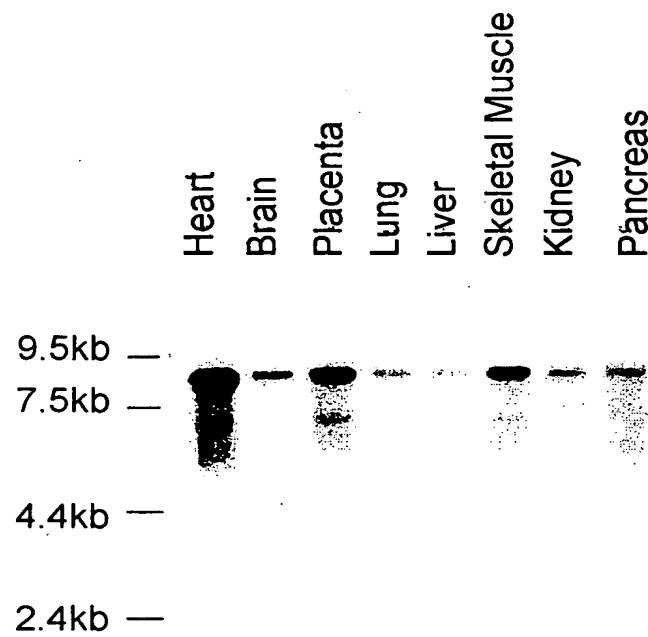
## FIG. 2

### Tth Expression Profile of huE3 $\alpha$ -II in Human Tissues

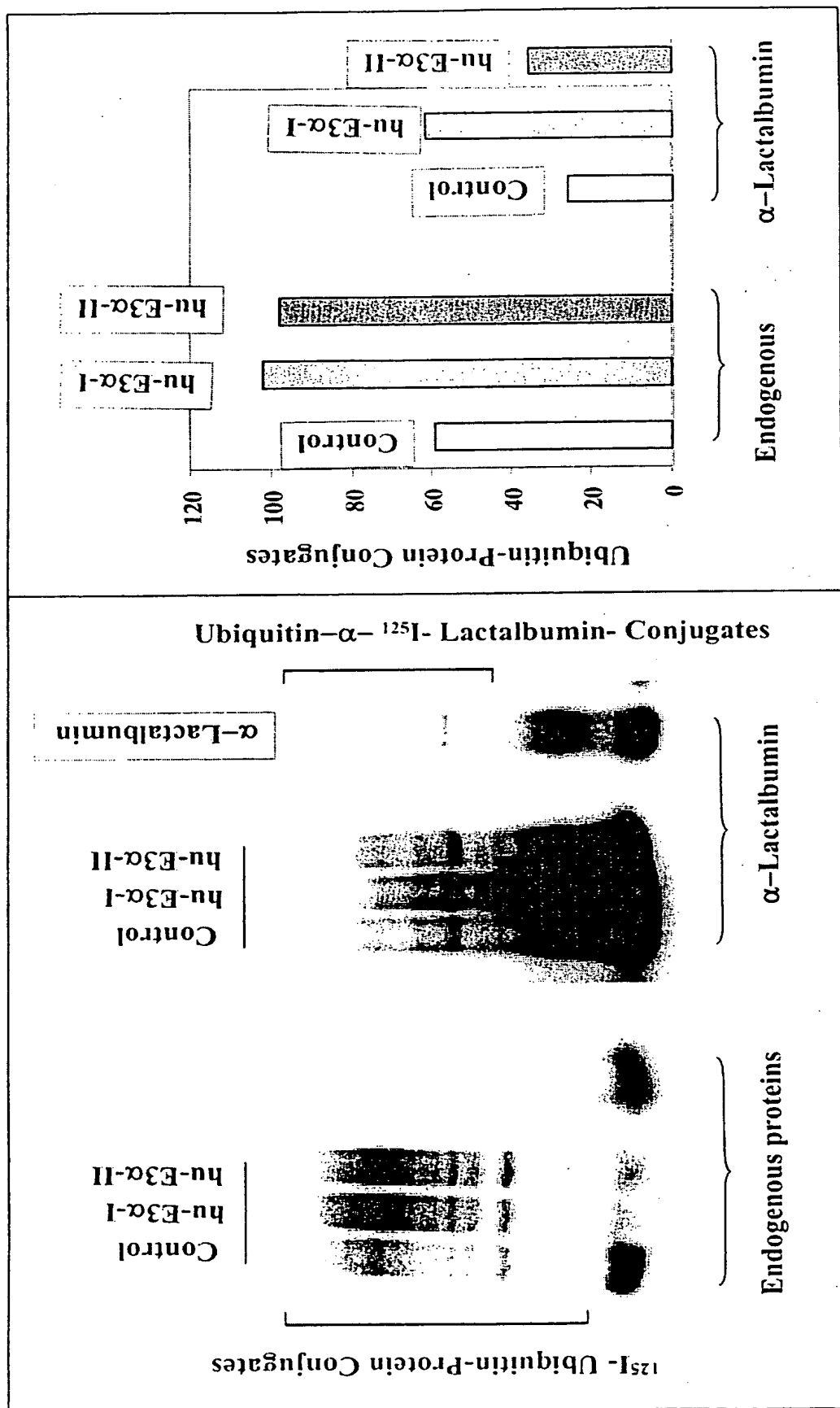


## FIG. 3

### Tth Expression Profile of huE3 $\alpha$ -I in Human Tissues

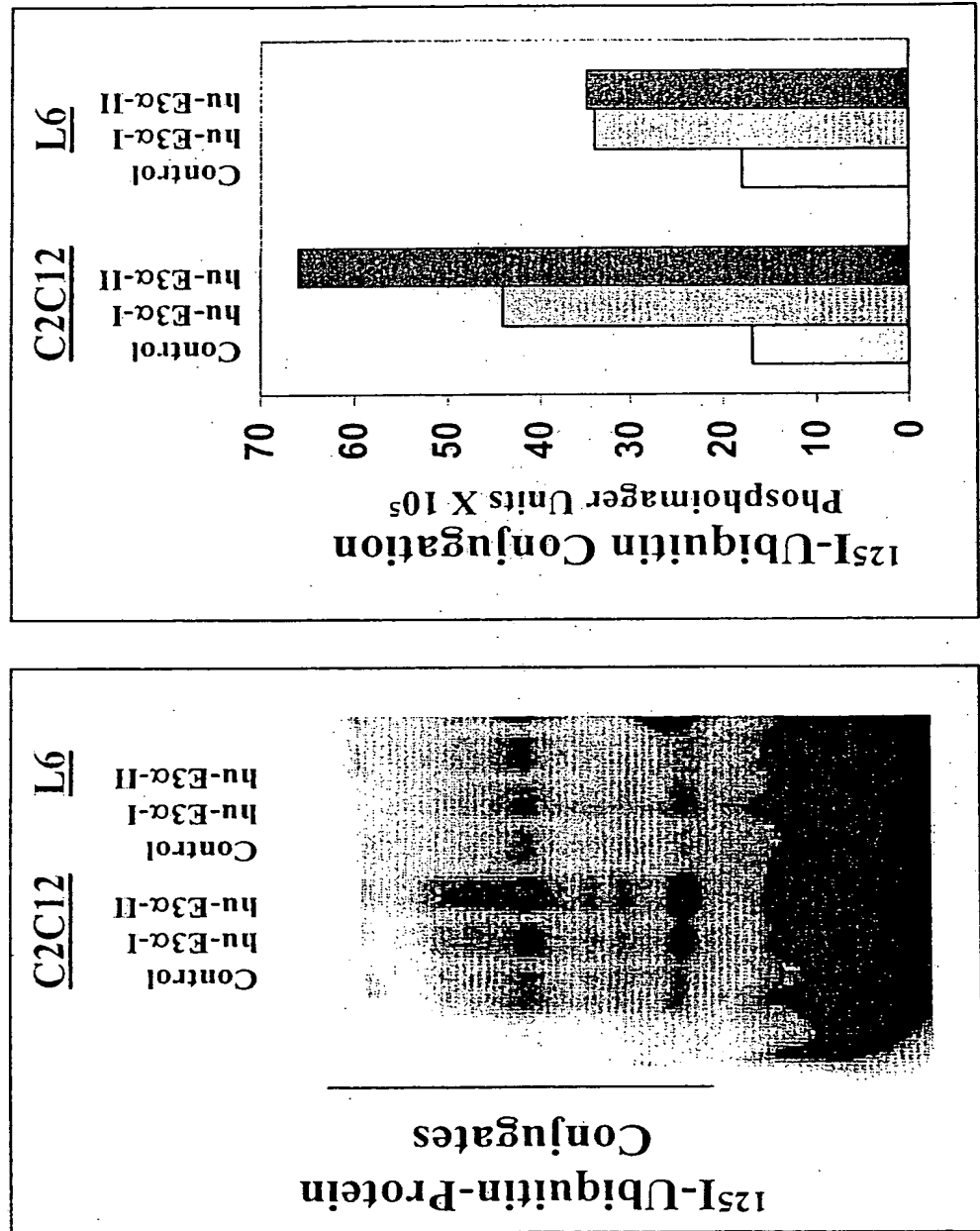


**Figure 4**  
**Ubiquitination of Endogenous Proteins**





**Figure 5**  
**Transfection of Human E3 $\alpha$ -I or E3 $\alpha$ -II cDNA Stimulates**  
**Ubiquitin Conjugation in Cultured Muscle Cell Lines**



**Figure 6**  
<sup>125</sup>I-Ubiquitin Conjugation to Muscle Proteins and Its Sensitivity to E3 $\alpha$  Inhibitor  
 in Skeletal Muscle Extracts

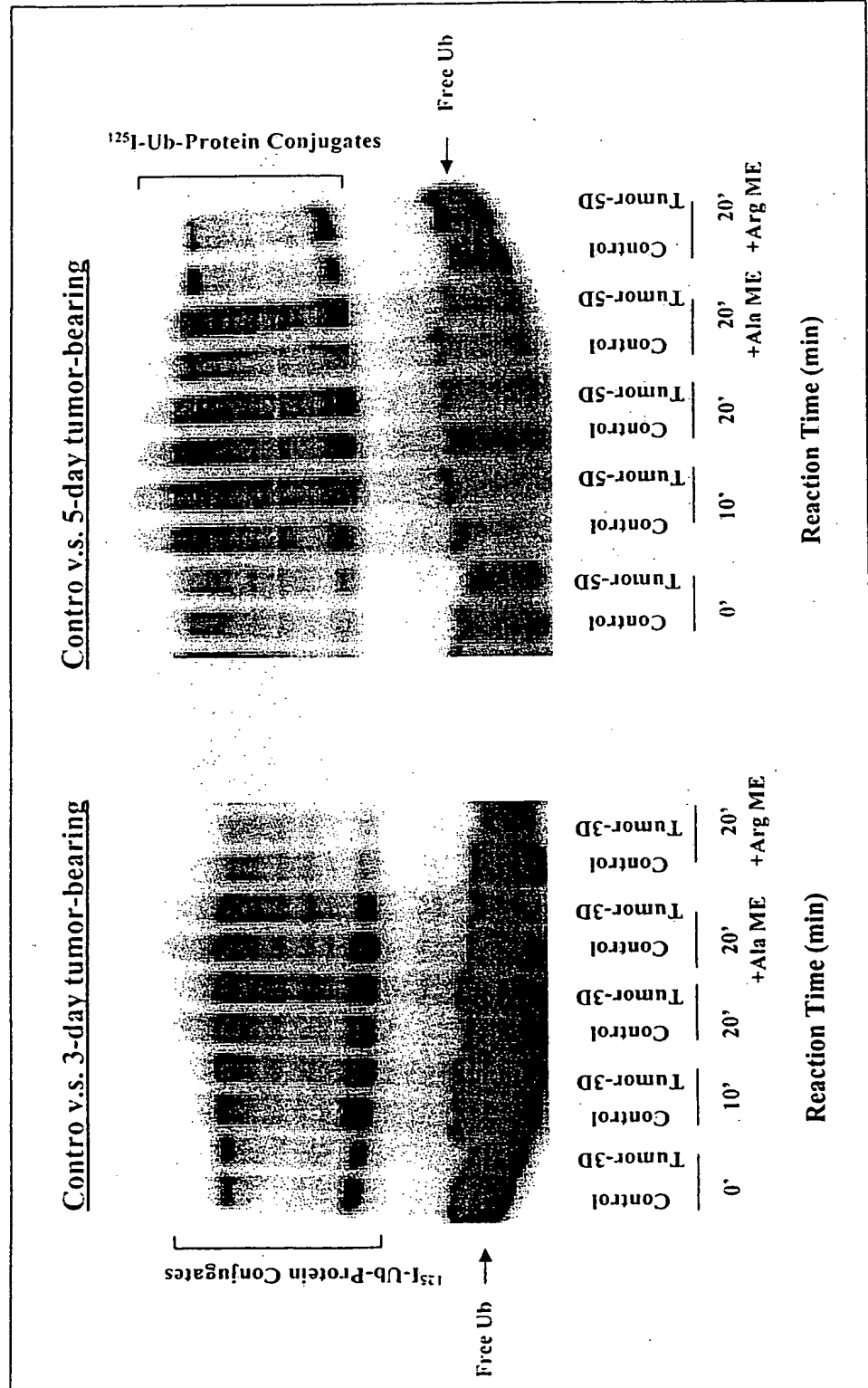
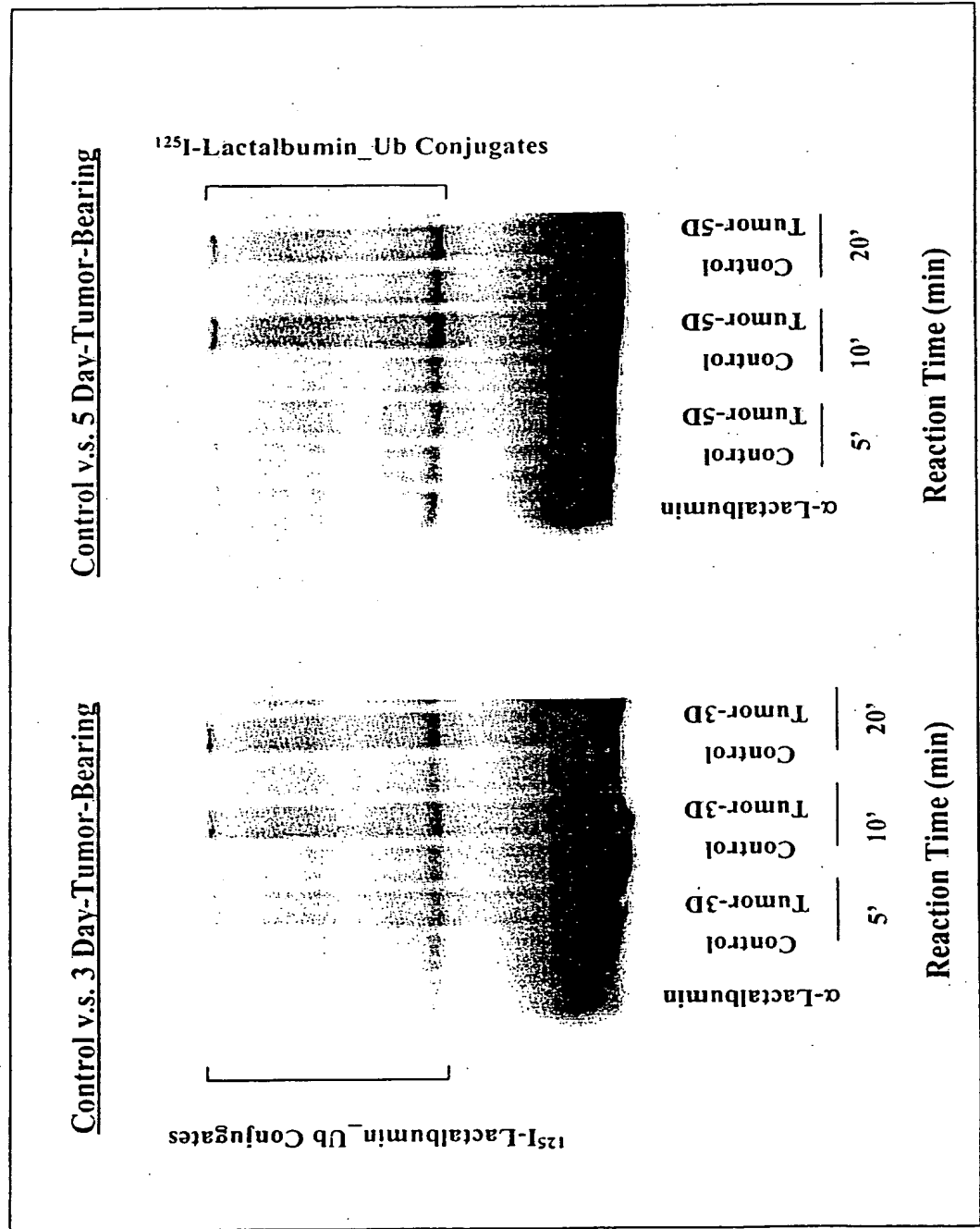
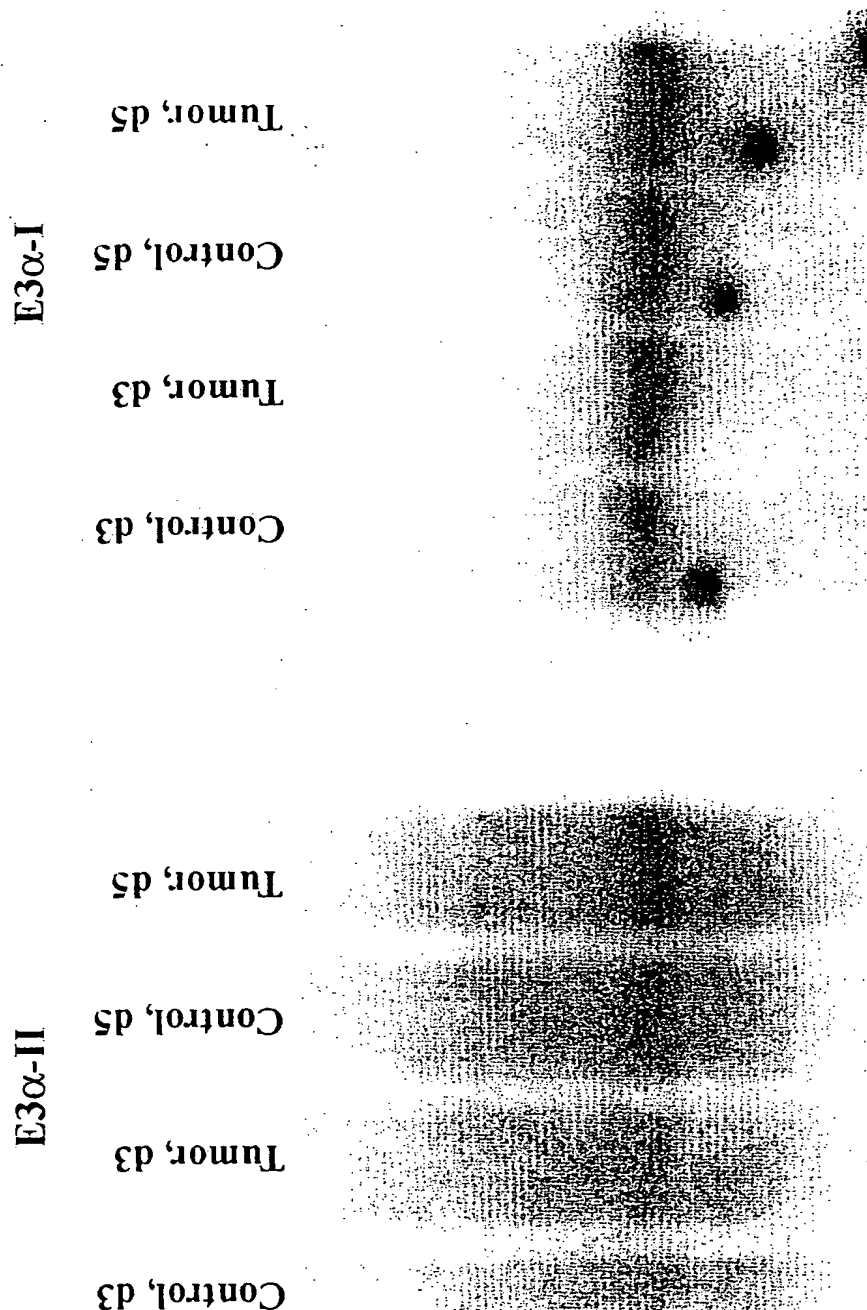


Figure 7  
 Rates of Ubiquitination of N-end Rule Substrate  
 $\alpha$ -Lactalbumin in Skeletal Muscle Extracts



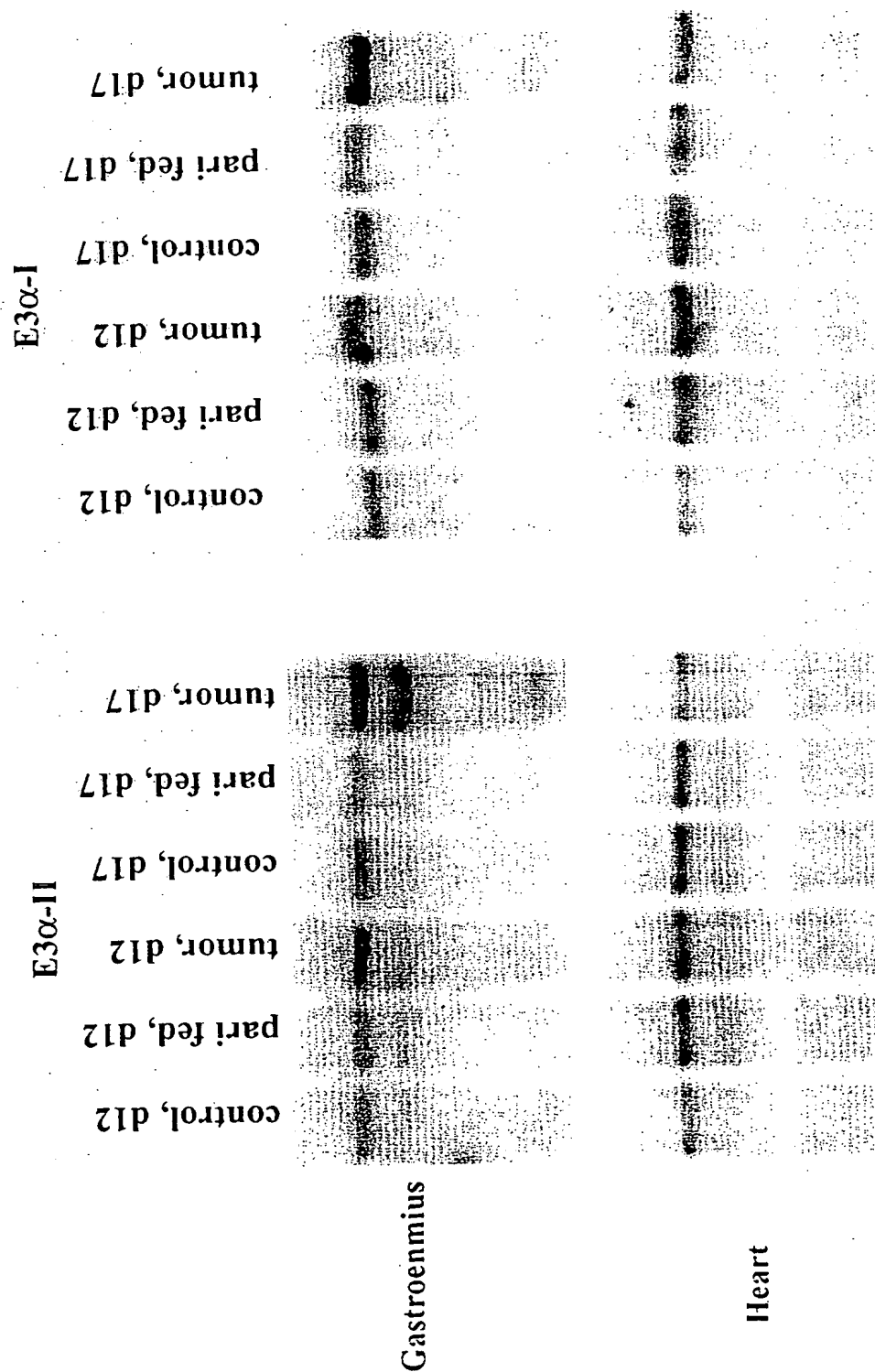
**Figure 8**

**Northern blot analysis of E3 $\alpha$ -I & E3 $\alpha$ -II expression  
in gastrocnemius muscles in YAH-130 experimental cachexia model**



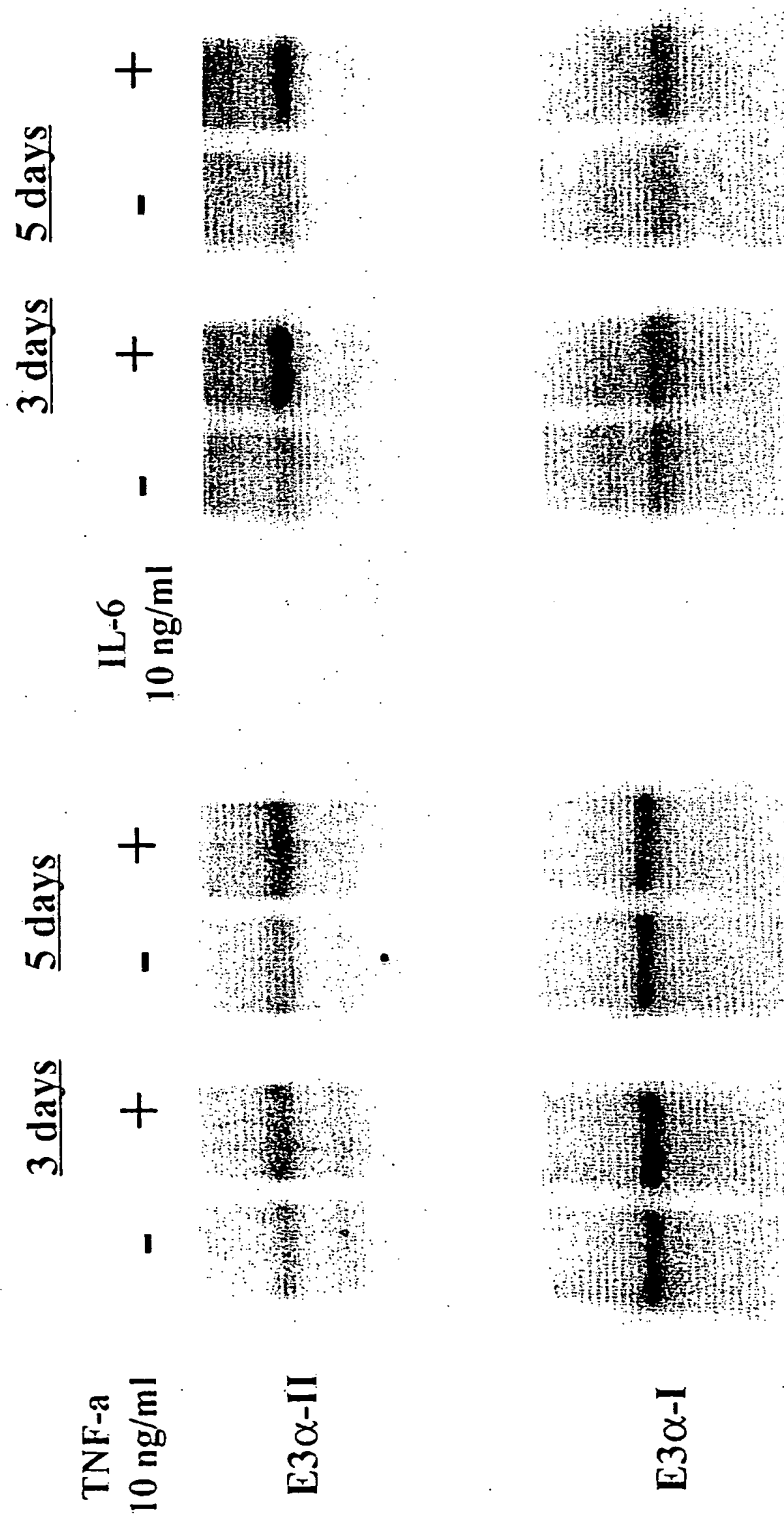
**Figure 9**

**Northern blot analysis of E3 $\alpha$ -I and E3 $\alpha$ -II expression in  
gastrocnemius muscle and cardiac muscle  
in C26 experimental cachexia model**

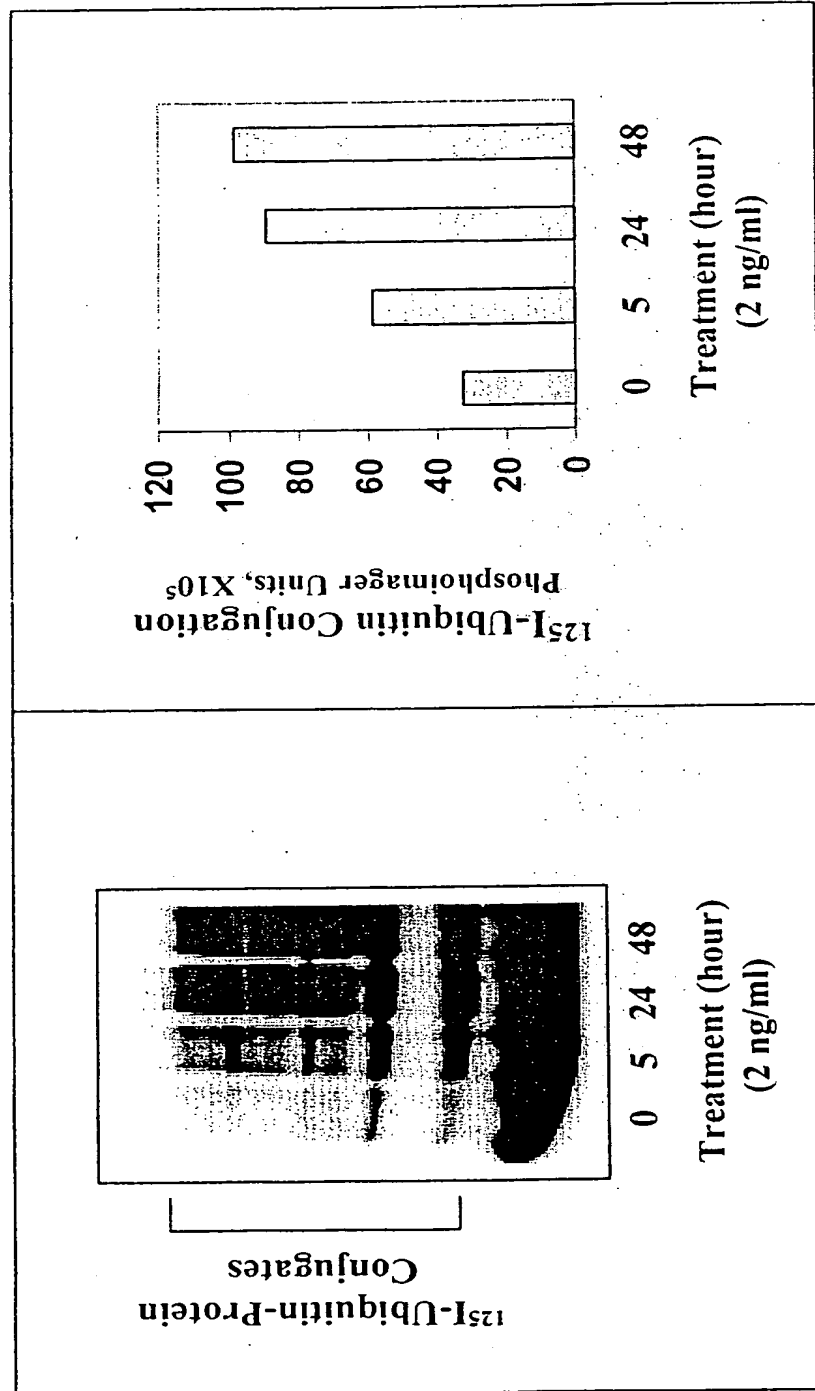


**Figure 10**

Proinflammatory cytokines TNF- $\alpha$  and IL-6  
induce E3 $\alpha$ -II Expression in C2C12 myotube culture



**Figure 11**  
**IL-6 Elicits Accelerated Ubiquitination in C2C12 Myotube Cultures**



**Figure 12**  
**TNF $\alpha$  Elicits Accelerated Ubiquitination in C2C12 Myotube Cultures**

